Please deduct all fees associated with this communication from Deposit Account No. 19-2090.

Respectfully submitted,

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Haplotype estimation was accomplished using a program from Max Delbruck Center for Molecular Medicine, Berlin at http://www.bioinf.mdc-berlin.de/projects/hap/ according to the website file format. Table 4 shows a haplotype description of the 12 SNAJA loci based on the sequence listing for SNAJA, SEQ ID NO:1. Table 7 shows the results of the SNAJA Haplotype estimation frequencies for dyslexic and non-dyslexic sample set, where 1 represents the wild type and 2 represents the positional variant.

TABLE 4

Haplotype Description of 12 SNAJA Loci Based

LOCUS	1	2	3	4	5	6	7	8	9	10	11	12
POSITION/ CHANGE	A424C	C554A	A879T	C985A	G1145A	C1346T	A2275G	A2286C	G2314A	C2453T	G2613A	T3282G
HAPLOTYPE WILD TYPE CODE	1	1	1	1	1	1	1	1	1	1	1	1
HAPLOTYPE VARIANT CODE	2	2	2	2	2	2	2	2	2	2	2	2

TABLE 5

Results of SNAJA Haplotype Estimation Frequencies

HAPLOTYPE	ESTIMATED 12 LOCI HAPLOTYPE	DYSLEXIC SAMPLES	NON-DYSLEXIC SAMPLES	GENERAL POPULATION SAMPLES
A	221112112121	0.295	0.250	0.241
B	111111111111	0.217	0.275	0.297
C	222112112121	0.200	0.275	0.300
D	111121111122	0.170	0.175	0.162
1	112111111121	0.083	0.000	0.000
2	221112122121	0.050	0.000	0.000
3	111121111121	0.061	0.000	0.000
4	221112112122	0.061	0.000	0.000
5	222112112122	0.050	0.000	0.000
6	112111111111	0.083	0.000	0.000
7	111111121121	0.050	0.000	0.000
E	112121211122	0.000	0.050	0.000

The finding that seven estimated 12 loci haplotypes (1, 2, 3, 4, 5, 6, 7) occurred in only the dyslexic population indicates that these haplotypes are associated with the risk of exhibiting dyslexia phenotypes, and that a variant form or forms of SNAJA is involved in the